

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WALLACH, David
BOLDIN, Mark
VARFOLOMEEV, Eugene
METT, Igor
- (ii) TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS/AP01
RECEPTORS
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
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 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: United States of America
 - (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/860,082
 - (B) FILING DATE: 19-AUG-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US95/16542
 - (B) FILING DATE: 14-DEC-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 112022
 - (B) FILING DATE: 15-DEC-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 112692
 - (B) FILING DATE: 19-FEB-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: IL 114615
 - (B) FILING DATE: 16-JUL-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BROWDY, Roger L.
 - (B) REGISTRATION NUMBER: 25,618
 - (C) REFERENCE/DOCKET NUMBER: WALLACH=16
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1701 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTG AAT CAG GCA CCG GAG TGC AGG TTC GGG GGT GGA ATC CTT GGG CCG	48
Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro	
1 5 10 15	
CTG GGC AAG CGG CGA GAC CTG GCC AGG GCC AGC GAG CCG AGG ACA GAG	96
Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu	
20 25 30	
GGC GCG CGG AGG GCC GGG CCG CAG CCC CGG CCG CTT GCA GAC CCC GCC	144
Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala	
35 40 45	
ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC AGC CTG TCG	192
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser	
50 55 60	
AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG CGC GTG GTC	240
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val	
65 70 75 80	
AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC TTC TCC ATG	288
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met	
85 90 95	
CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG CTC CTG CGC	336
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg	
100 105 110	
GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG CGC GTC GAC	384
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp	
115 120 125	
GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG GAA GAA GAC	432
Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp	
130 135 140	
CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG AAA GAT TGG	480
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp	
145 150 155 160	
AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG ATC GAC AGC	528
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser	
165 170 175	
ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG CGG GAG TCA	576
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser	
180 185 190	
CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA GTG GCC CAC	624
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His	
195 200 205	
CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG GCT GAC CTG	672
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu	
210 215 220	
GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG AGT GGG GCC	720
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala	
225 230 235 240	

ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC GAA GCG TCC 768
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
245 250 255

TGATGGGCGG CTGCTTTGCG CTGGTGGACC ACAGGCATCT ACACAGCCTG GACTTTGGTT 828
CTCTCCAGGA AGGTAGCCCA GCACTGTGAA GACCCAGCAG GAAGCCAGGC TGAGTGAGCC 888
ACAGACCACC TGCTTCTGAA CTCAAGCTGC GTTTATTAAT GCCTCTCCCG CACCAGGCCG 948
GGCTTGGGCC CTGCACAGAT ATTTCCATTT CTTCTCACT ATGACACTGA GCAAGATCTT 1008
GTCTCCACTA AATGAGCTCC TGCGGGAGTA GTTGGAAAGT TGAACCGTG TCCAGCACAG 1068
AAGGAATCTG TGCAGATGAG CAGTCACACT GTTACTCCAC AGCGGAGGAG ACCAGCTCAG 1128
AGGCCCAGGA ATCGGAGCGA AGCAGAGAGG TGGAGAACTG GGATTTGAAC CCCC GCCATC 1188
CTTCACCAGA GCCCATGCTC AACCCTGTG GCGTTCTGCT GCCCTGCGAG TTGGCAGAAA 1248
GGATGTTTTT GTCCCATTTT CTTGGAGGCC ACCGGGACAG ACCTGGACAC TAGGGTCAGG 1308
CGGGGTGCTG TGGTGGGGAG AGGCATGGCT GGGGTGGGGG TGGGGAGACC TGGTTGGCCG 1368
TGGTCCAGCT CTTGGCCCCCT GTGTGAGTTG AGTCTCTCT CTGAGACTGC TAAGTAGGGG 1428
CAGTGATGGT TGCCAGGACG AATTGAGATA ATATCTGTGA GGTGCTGATG AGTGATTGAC 1488
ACACAGCACT CTCTAAATCT TCCTTGTGAG GATTATGGGT CCTGCAATTC TACAGTTTCT 1548
TACTGTTTTG TATCAAAAATC ACTATCTTTC TGATAACAGA ATTGCCAAGG CAGCGGGATC 1608
TCGTATCTTT AAAAAGCAGT CCTCTTATTC CTAAGGTAAT CCTATTAAAA CACAGCTTTA 1668
CAACTTCCAT ATTACAAAAA AAAAAAAAAA AAA 1701

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
1 5 10 15
Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
20 25 30
Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
35 40 45
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
50 55 60
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
65 70 75 80
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
85 90 95

Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
 100 105 110
 Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
 115 120 125
 Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
 130 135 140
 Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
 145 150 155 160
 Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
 165 170 175
 Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
 180 185 190
 Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
 195 200 205
 Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
 210 215 220
 Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
 225 230 235 240
 Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
 245 250 255